

SEQUENCE LISTING

<110> NISHIDA, Yoshihiro
OKURA, Takanori
TANIMOTO, Tadao
KURIMOTO, Masashi

<120> PEPTIDE

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<150> JP 177,580/98
<151> 1998-6-24

<150> JP 289,044/98
<151> 1998-10-12

<150> JP 365,023/98
<151> 1998-12-22

<160> 33

<210> 1
<211> 108
<212> PRT
<213> Mus musculus

<400> 1

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Gly
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Glu	Arg	Val	Ser	Leu	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Gly	Ser	Lys
		20						25					30		

Leu	Tyr	Trp	Leu	Gln	Gln	Glu	Pro	Asp	Gly	Thr	Phe	Lys	Arg	Leu	Ile
	35						40					45			

Tyr	Ala	Thr	Ser	Ser	Leu	Asp	Ser	Gly	Val	Pro	Lys	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Arg	Ser	Gly	Ser	Asp	Tyr	Ser	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Ser
65					70					75				80	

Glu	Asp	Phe	Val	Asp	Tyr	Tyr	Cys	Leu	Gln	Tyr	Ala	Ser	Ser	Pro	Tyr
			85						90					95	

Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Ala	Ile	Lys	Arg
		100						105			

<210> 2
<211> 113
<212> PRT
<213> Mus musculus

<400> 2

Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
20 25 30

Phe Ile Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Arg Asp Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Thr Thr Ala Phe
65 70 75 80

Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Gly Leu Arg Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ala

<210> 3

<211> 11

<212> PRT

<213> Mus musculus

<400> 3

Arg Ala Ser Gln Asp Ile Gly Ser Lys Leu Tyr
1 5 10

<210> 4

<211> 7

<212> PRT

<213> Mus musculus

<400> 4

Ala Thr Ser Ser Leu Asp Ser
1 5

<210> 5

<211> 9

<212> PRT

<213> Mus musculus

<400> 5

Leu Gln Tyr Ala Ser Ser Pro Tyr Thr
1 5

<210> 6

<211> 10

<212> PRT

<213> Mus musculus

<400> 6

Gly Tyr Ser Phe Thr Asp Tyr Phe Ile Tyr
1 5 10

<210> 7

<211> 17

<212> PRT

<213> Mus musculus

<400> 7

Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Arg
1 5 10 15

Asp

<210> 8

<211> 4

<212> PRT

<213> Mus musculus

<400> 8

Gly Leu Arg Phe
1

<210> 9

<211> 237

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificially produced peptide in the form of a single chain
variable region fragment (scFv) which neutralizes IL-18

<400> 9

Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
20 25 30

Phe Ile Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Arg Asp Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Thr Thr Ala Phe
65 70 75 80

Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Gly Leu Arg Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ala Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
130 135 140

Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly
145 150 155 160

Ser Lys Leu Tyr Trp Leu Gln Gln Glu Pro Asp Gly Thr Phe Lys Arg
165 170 175

Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe
180 185 190

Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu
195 200 205

Glu Ser Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser
210 215 220

Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Ala Ile Lys
225 230 235

<210> 10

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificially produced peptide in the form of a single chain variable region fragment (scFv) which neutralizes IL-18

<400> 10

Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
20 25 30

Phe Ile Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Arg Asp Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Thr Thr Ala Phe
65 70 75 80

Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Gly Leu Arg Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ala Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
130 135 140

Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly
145 150 155 160

Ser Lys Leu Tyr Trp Leu Gln Gln Glu Pro Asp Gly Thr Phe Lys Arg
165 170 175

Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe
180 185 190

Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu
195 200 205

Glu Ser Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser
210 215 220

Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Ala Ile Lys His His His
225 230 235 240

His His His

<210> 11

<211> 324

<212> DNA

<213> Mus musculus

<400> 11

gac atc cag atg acc cag tct cca tcc tcc tta tct gcc tct ctg gga 48
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

gaa aga gtc agt ctc act tgt cgg gca agt cag gac att ggt agt aaa 96
Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly Ser Lys
20 25 30

tta tac tgg ctt caa cag gaa cca gat gga act ttt aaa cgc ctg atc 144
Leu Tyr Trp Leu Gln Gln Glu Pro Asp Gly Thr Phe Lys Arg Leu Ile
35 40 45

tac gcc aca tcc agt tta gat tct ggt gtc ccc aag agg ttc agt ggc 192
Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
50 55 60

agt agg tct ggg tca gat tat tct ctc acc atc agc agc ctt gag tct 240
Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

gaa gat ttt gta gac tat tac tgt cta caa tat gct agt tct ccg tac 288
 Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser Pro Tyr
 85 90 95

acg ttc gga ggg ggg acc aag ctg gca ata aaa cgg 324
 Thr Phe Gly Gly Gly Thr Lys Leu Ala Ile Lys Arg
 100 105

<210> 12
 <211> 339
 <212> DNA
 <213> Mus musculus

<400> 12
 gag atc cag ctg cag cag tct gga cct gag ctg gtg aag cct ggg gct 48
 Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

tca gtg aag gtc tcc tgt aag gct tct ggt tac tca ttc act gac tac 96
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
 20 25 30

ttc att tac tgg gtg aag cag agc cat gga aag agc ctt gag tgg att 144
 Phe Ile Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45

gga gat att gat cct tat aat ggt gat act agt tac aac cag aag ttc 192
 Gly Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

agg gac aag gcc aca ttg act gtt gac cag tcc tcc acc aca gcc ttc 240
 Arg Asp Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Thr Thr Ala Phe
 65 70 75 80

atg cat ctc aac agc ctg aca tct gag gac tct gca gtc tat ttc tgt 288
 Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95

gca aga ggc cta cgg ttc tgg ggc caa ggg act ctg gtc act gtc tct 336
 Ala Arg Gly Leu Arg Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 100 105 110

gca 339
 Ala

<210> 13
 <211> 33
 <212> DNA
 <213> Mus musculus

<400> 13
 cgg gca agt cag gac att ggt agt aaa tta tac 33
 Arg Ala Ser Gln Asp Ile Gly Ser Lys Leu Tyr
 1 5 10

<210> 14
 <211> 21
 <212> DNA
 <213> Mus musculus

<400> 14
 gcc aca tcc agt tta gat tct 21
 Ala Thr Ser Ser Leu Asp Ser
 1 5

<210> 15
 <211> 27
 <212> DNA
 <213> Mus musculus

<400> 15
 cta caa tat gct agt tct ccg tac acg 27
 Leu Gln Tyr Ala Ser Ser Pro Tyr Thr
 1 5

<210> 16
 <211> 30
 <212> DNA
 <213> Mus musculus

<400> 16
 ggt tac tca ttc act gac tac ttc att tac 30
 Gly Tyr Ser Phe Thr Asp Tyr Phe Ile Tyr
 1 5 10

<210> 17
 <211> 51
 <212> DNA
 <213> Mus musculus

<400> 17
 gat att gat cct tat aat ggt gat act agt tac aac cag aag ttc agg 48
 Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Arg
 1 5 10 15

gac 51
 Asp

<210> 18
 <211> 12
 <212> DNA
 <213> Mus musculus

<400> 18
 ggc cta cgg ttc 12
 Gly Leu Arg Phe
 1

<210> 19
 <211> 711

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial DNA to code for the amino acid sequence of SEQ
ID NO:9

<400> 19

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gag atc cag ctg cag cag tct gga cct gag ctg gtg aag cct ggg gct 48
Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
  1             5             10             15

tca gtg aag gtc tcc tgt aag gct tct ggt tac tca ttc act gac tac 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
      20             25             30

ttc att tac tgg gtg aag cag agc cat gga aag agc ctt gag tgg att 144
Phe Ile Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
      35             40             45

gga gat att gat cct tat aat ggt gat act agt tac aac cag aag ttc 192
Gly Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
      50             55             60

agg gac aag gcc aca ttg act gtt gac cag tcc tcc acc aca gcc ttc 240
Arg Asp Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Thr Thr Ala Phe
      65             70             75             80

atg cat ctc aac agc ctg aca tct gag gac tct gca gtc tat ttc tgt 288
Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
      85             90             95

gca aga ggc cta cgg ttc tgg ggc caa ggg act ctg gtc act gtc tct 336
Ala Arg Gly Leu Arg Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser
      100             105             110

gca ggt gga ggt gga ggc gga tcc ggc gga ggt ggc tct ggc ggt ggc 384
Ala Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
      115             120             125

gga tcg gac atc cag atg acc cag tct cca tcc tcc tta tct gcc tct 432
Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
      130             135             140

ctg gga gaa aga gtc agt ctc act tgt cgg gca agt cag gac att ggt 480
Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly
      145             150             155             160

agt aaa tta tac tgg ctt caa cag gaa cca gat gga act ttt aaa cgc 528
Ser Lys Leu Tyr Trp Leu Gln Gln Glu Pro Asp Gly Thr Phe Lys Arg
      165             170             175

ctg atc tac gcc aca tcc agt tta gat tct ggt gtc ccc aag agg ttc 576
Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe
      180             185             190
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agt ggc agt agg tct ggg tca gat tat tct ctc acc atc agc agc ctt 624
 Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu
 195 200 205

gag tct gaa gat ttt gta gac tat tac tgt cta caa tat gct agt tct 672
 Glu Ser Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser
 210 215 220

ccg tac acg ttc gga ggg ggg acc aag ctg gca ata aaa 711
 Pro Tyr Thr Phe Gly Gly Thr Lys Leu Ala Ile Lys
 225 230 235

<210> 20
 <211> 729
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial DNA to code for the amino acid sequence of SEQ
 ID NO:10

<400> 20
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 Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

tca gtg aag gtc tcc tgt aag gct tct ggt tac tca ttc act gac tac 96
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
 20 25 30

ttc att tac tgg gtg aag cag agc cat gga aag agc ctt gag tgg att 144
 Phe Ile Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
 35 40 45

gga gat att gat cct tat aat ggt gat act agt tac aac cag aag ttc 192
 Gly Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

agg gac aag gcc aca ttg act gtt gac cag tcc tcc acc aca gcc ttc 240
 Arg Asp Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Thr Thr Ala Phe
 65 70 75 80

atg cat ctc aac agc ctg aca tct gag gac tct gca gtc tat ttc tgt 288
 Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95

gca aga ggc cta cgg ttc tgg ggc caa ggg act ctg gtc act gtc tct 336
 Ala Arg Gly Leu Arg Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 100 105 110

gca ggt gga ggt gga ggc gga tcc ggc gga ggt ggc tct ggc ggt ggc 384
 Ala Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

gga tcg gac atc cag atg acc cag tct cca tcc tcc tta tct gcc tct 432

Gly	Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser		
130						135					140						
ctg	gga	gaa	aga	gtc	agt	ctc	act	tgt	cgg	gca	agt	cag	gac	att	ggc	480	
Leu	Gly	Glu	Arg	Val	Ser	Leu	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Gly		
145					150				155						160		
agt	aaa	tta	tac	tgg	ctt	caa	cag	gaa	cca	gat	gga	act	ttt	aaa	cgc	528	
Ser	Lys	Leu	Tyr	Trp	Leu	Gln	Gln	Glu	Pro	Asp	Gly	Thr	Phe	Lys	Arg		
				165				170						175			
ctg	atc	tac	gcc	aca	tcc	agt	tta	gat	tct	ggc	gtc	ccc	aag	agg	ttc	576	
Leu	Ile	Tyr	Ala	Thr	Ser	Ser	Leu	Asp	Ser	Gly	Val	Pro	Lys	Arg	Phe		
			180					185						190			
agt	ggc	agt	agg	tct	ggg	tca	gat	tat	tct	ctc	acc	atc	agc	agc	ctt	624	
Ser	Gly	Ser	Arg	Ser	Gly	Ser	Asp	Tyr	Ser	Leu	Thr	Ile	Ser	Ser	Leu		
		195				200					205						
gag	tct	gaa	gat	ttt	gta	gac	tat	tac	tgt	cta	caa	tat	gct	agt	tct	672	
Glu	Ser	Glu	Asp	Phe	Val	Asp	Tyr	Tyr	Cys	Leu	Gln	Tyr	Ala	Ser	Ser		
		210				215					220						
cgc	tac	acg	ttc	gga	ggg	ggg	acc	aag	ctg	gca	ata	aaa	cat	cac	cat	720	
Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Ala	Ile	Lys	His	His	His		
225					230				235						245		
cac	cat	cac														729	
His	His	His															

<210> 21
 <211> 157
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE
 <222> (73)
 <223> "Xaa" means an amino acid of isoleucine or threonine.

<400> 21
 Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn
 1 5 10 15
 Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp
 20 25 30
 Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile
 35 40 45
 Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile
 50 55 60
 Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys Glu Asn Lys Ile

65	70	75	80
Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys	85	90	95
Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys	100	105	110
Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu	115	120	125
Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu	130	135	140
Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp	145	150	155

<210> 22
 <211> 157
 <212> PRT
 <213> Mus Musculus

 <220>
 <221> UNSURE
 <222> (70)
 <223> "Xaa" means an amino acid of methionine or threonine.

 <400> 22

Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg Asn Ile Asn	1	5	10	15
Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe Glu Asp Met	20	25	30	
Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg Leu Ile Ile	35	40	45	
Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val Thr Leu Ser	50	55	60	
Val Lys Asp Ser Lys Xaa Ser Thr Leu Ser Cys Lys Asn Lys Ile Ile	65	70	75	80
Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp Ile Gln Ser	85	90	95	
Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn Lys Met Glu	100	105	110	
Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys Gln Lys Glu	115	120	125	
Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp	130	135	140	

Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser
 145 150 155

<210> 23
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide as sense primer to amplify a cDNA
 fragment coding for an antibody light chain variable region

<400> 23
 actagtcgac atgaggrccc ctgctcagwt tyttggmwtc ttg 43

<210> 24
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide as antisense primer to amplify a cDNA
 fragment coding for an antibody light chain variable region

<400> 24
 ggatcccggg tggatggtgg gaagatg 27

<210> 25
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide as sense primer to amplify a cDNA
 fragment coding for an antibody heavy chain variable region

<400> 25
 actagtcgac atggratgga gckggrtctt tmtctt 36

<210> 26
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide as antisense primer to amplify a cDNA
 fragment coding for an antibody heavy chain variable region

<400> 26
 ggatcccggg ccagtggata gacagatg 28

<210> 27
 <211> 407
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(407)

<220>
 <221> sig peptide
 <222> (1)...(60)

<400> 27

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Met	Arg	Ala	Pro	Ala	Gln	Ile	Phe	Gly	Phe	Leu	Leu	Leu	Leu	Phe	Pro	
1				5				10						15		

ggc	acc	aga	tgt	gac	atc	cag	atg	acc	cag	tct	cca	tcc	tcc	tta	tct	96
Gly	Thr	Arg	Cys	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	
			20					25					30			

gcc	tct	ctg	gga	gaa	aga	gtc	agt	ctc	act	tgt	cgg	gca	agt	cag	gac	144
Ala	Ser	Leu	Gly	Glu	Arg	Val	Ser	Leu	Thr	Cys	Arg	Ala	Ser	Gln	Asp	
			35				40					45				

att	ggc	agt	aaa	tta	tac	tgg	ctt	caa	cag	gaa	cca	gat	gga	act	ttt	192
Ile	Gly	Ser	Lys	Leu	Tyr	Trp	Leu	Gln	Gln	Glu	Pro	Asp	Gly	Thr	Phe	
			50				55					60				

aaa	cgc	ctg	atc	tac	gcc	aca	tcc	agt	tta	gat	tct	ggc	gtc	ccc	aag	240
Lys	Arg	Leu	Ile	Tyr	Ala	Thr	Ser	Ser	Leu	Asp	Ser	Gly	Val	Pro	Lys	
65					70					75				80		

agg	ttc	agt	ggc	agt	agg	tct	ggg	tca	gat	tat	tct	ctc	acc	atc	agc	288
Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Ser	Asp	Tyr	Ser	Leu	Thr	Ile	Ser	
				85				90						95		

agc	ctt	gag	tct	gaa	gat	ttt	gta	gac	tat	tac	tgt	cta	caa	tat	gct	336
Ser	Leu	Glu	Ser	Glu	Asp	Phe	Val	Asp	Tyr	Tyr	Cys	Leu	Gln	Tyr	Ala	
			100				105					110				

agt	tct	ccg	tac	acg	ttc	gga	ggg	ggg	acc	aag	ctg	gca	ata	aaa	cgg	384
Ser	Ser	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Ala	Ile	Lys	Arg	
		115				120						125				

gct	gat	gct	gca	cca	act	gta	tc									407
Ala	Asp	Ala	Ala	Pro	Thr	Val										
		130				135										

<210> 28
 <211> 412
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(412)

<220>

<221> sig peptide

<222> (1)...(60)

<400> 28

atg gga tgg agc ggg atc ttt ctc ttc ctc ctg tca gga cct aca ggt	48
Met Gly Trp Ser Gly Ile Phe Leu Phe Leu Leu Ser Gly Pro Thr Gly	
1 5 10 15	

gtc cac tct gag atc cag ctg cag cag tct gga cct gag ctg gtg aag	96
Val His Ser Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys	
20 25 30	

cct ggg gct tca gtg aag gtc tcc tgt aag gct tct ggt tac tca ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe	
35 40 45	

act gac tac ttc att tac tgg gtg aag cag agc cat gga aag agc ctt	192
Thr Asp Tyr Phe Ile Tyr Trp Val Lys Gln Ser His Gly Lys Ser Leu	
50 55 60	

gag tgg att gga gat att gat cct tat aat ggt gat act agt tac aac	240
Glu Trp Ile Gly Asp Ile Asp Pro Tyr Asn Gly Asp Thr Ser Tyr Asn	
65 70 75 80	

cag aag ttc agg gac aag gcc aca ttg act gtt gac cag tcc tcc acc	288
Gln Lys Phe Arg Asp Lys Ala Thr Leu Thr Val Asp Gln Ser Ser Thr	
85 90 95	

aca gcc ttc atg cat ctc aac agc ctg aca tct gag gac tct gca gtc	336
Thr Ala Phe Met His Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val	
100 105 110	

tat ttc tgt gca aga ggc cta cgg ttc tgg ggc caa ggg act ctg gtc	384
Tyr Phe Cys Ala Arg Gly Leu Arg Phe Trp Gly Gln Gly Thr Leu Val	
115 120 125	

act gtc tct gca gcc aaa acg aca ccc c	412
Thr Val Ser Ala Ala Lys Thr Thr Pro	
130 135	

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<220>

<223> Designed oligonucleotide as sense primer to amplify a DNA fragment containing the nucleotide sequence of SEQ ID NO:12

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43

<210> 31

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NO:11

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31

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45